RAW SEQUENCE LISTING   DATE: 06/18/2001
PATENT APPLICATION: US/09/857,008   TIME: 16:19:31

Input Set : A:\ES.txt
Output Set: N:\CRF3\06182001\I857008.raw

Does Not Comply
Correct [Diskette] Not... (handwritten)

```
 3  <110> APPLICANT: Herscovici, Jean
 4          Hofland, Hans
 5          Jacopin, Christophe
 6          Scherman, Daniel
 8  <120> TITLE OF INVENTION: NOVEL NUCLEIC ACID TRANSFERRING AGENTS, COMPOSITIONS
CONTAINING THEM AND
 9          USES
11  <130> FILE REFERENCE: ST98046PCT-US
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C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/857,008
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14  <141> CURRENT FILING DATE: 2001-05-30
16  <150> PRIOR APPLICATION NUMBER: PCT/FR99/02995
17  <151> PRIOR FILING DATE: 1999-12-02
19  <150> PRIOR APPLICATION NUMBER: US 60/117,184
20  <151> PRIOR FILING DATE: 1999-01-26
22  <150> PRIOR APPLICATION NUMBER: FR 98/15,309
23  <151> PRIOR FILING DATE: 1998-12-03
25  <160> NUMBER OF SEQ ID NOS: 2
27  <170> SOFTWARE: PatentIn version 3.0
29  <210> SEQ ID NO: 1
30  <211> LENGTH: 9
31  <212> TYPE: PRT
32  <213> ORGANISM: (none) [encoded] (handwritten)
34  <400> SEQUENCE: 1
36  Lys Thr Pro Lys Lys Ala Lys Lys Pro
37  1               5
39  <210> SEQ ID NO: 2
40  <211> LENGTH: 8
41  <212> TYPE: PRT
42  <213> ORGANISM: (none) [encoded] (handwritten)
44  <400> SEQUENCE: 2
45  Ala Thr Pro Ala Lys Lys Ala Ala
46  1               5
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(handwritten) *Per 1.823 f Sequence Rules, see item 10 on Error Summary Sheet*

VERIFICATION SUMMARY   DATE: 06/18/2001
PATENT APPLICATION: US/09/857,008   TIME: 16:10:32

Input Set : A:\ES.txt
Output Set : N:\CRF3\06182001\I857008.raw

1:13 M:270 C: Current Application Number differs. Replaced Current Application Number

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/837,003_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 _____ Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)